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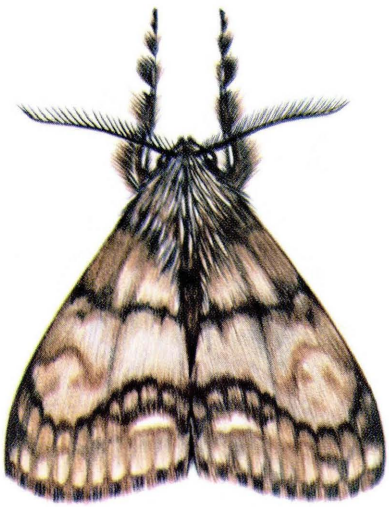
Douglas-Fir Tussock Moth Handbook

How to Sample Douglas-fir Tussock Moth Larvae



How to Sample Douglas-Fir Tussock Moth Larvae

by Richard R. Mason[1]

Introduction

In 1974 the U.S. Department of Agriculture initiated the Combined Forest Pest Research and Development Program, an interagency effort that concentrated on the Douglas-fir tussock moth in the West, on the southern pine beetle in the South, and on the gypsy moth in the Northeast. The work reported in this publication was funded in whole or in part by the Program. This manual is one in a series on the Douglas-fir tussock moth.

The potential for damage caused by the Douglas-fir tussock moth in western forests is measured by the number of larvae present. The intensity of tree defoliation is directly related to the number of feeding caterpillers. Decisions about whether or not to control an outbreak are almost always based on a larval census and a subsequent estimate of expected damage. An estimate of larval numbers is also necessary in many research studies, such as when evaluating population trends and the effects of natural factors or insecticides on tussock moth populations.

Obviously, it is impossible to count every larva in the forest. Instead, the number of larvae is estimated by selecting a sample of the population. Samples are relatively easy to collect and if properly selected can tell a great deal about the population.

Sampling is only a way of estimating the present number of larvae, however, and is not in itself a predictor of population trends.

Larval numbers are expressed in terms of the number of larvae per 1,000 inch^2 of branch area on the host tree. Such expressions of larval density are the basis of all numerical descriptions of tussock moth populations.

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Sampling Methods

Sampling is used either: (1) to estimate the precise density of larvae or (2) to classify the number of larvae into a general density category. Precise estimates are required in most research studies and for evaluating population trends or predicting tree damage. Simple classifications of density, however, are frequently adequate for surveys and may be all the information a forest manager needs to make some kinds of decisions. A classification of density into a high or low category can usually be made much cheaper and easier than precise estimates.

The sampling method is determined by the status of the tussock moth population and the purpose for which the sampling information is to be used. Guidelines for choosing the appropriate sampling scheme are provided along with the recommended procedures. Additional information is available in the references listed.

Where to Sample

Larvae of the tussock moth are found in all parts of the infested tree crown, but they are usually more concentrated in the top and toward the tips of the branches. The most accurate method for estimating larval density is to count the number of larvae on whole branch samples from several levels in the crown. Then the average density of larvae in the whole tree can be determined. Sampling all crown levels, however, is usually impractical except for the most detailed research projects.

A simpler method is to sample only parts of branches from just the middle portion of the tree crown. Since the highest larval densities are in the top of the crown and the lowest densities in the bottom, the midcrown density is fairly representative of the entire tree. The average density of larvae in the midcrown is, therefore, a useful index of the total number of larvae present in the population.

Because of the limited height of pole pruners used to clip branches, trees selected for sampling are usually less than 50 feet tall. Although these trees should have larval densities that are representative of the stand, estimates may have an unknown bias if many large trees are present that cannot be sampled.

Estimating Larval Density

The density of larvae in the midcrown can be estimated directly by sampling the midcrown or indirectly by sampling the lower crown. Midcrown sampling is recommended whenever larvae are fairly common, that is, at least 25 percent of the branches are infested. Lower crown sampling is suggested only as a quick census method for nonoutbreak or sparse populations where a large amount of foliage must be examined to find any larvae at all.

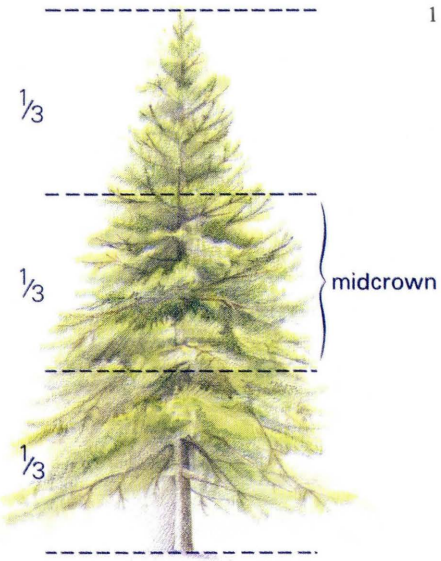


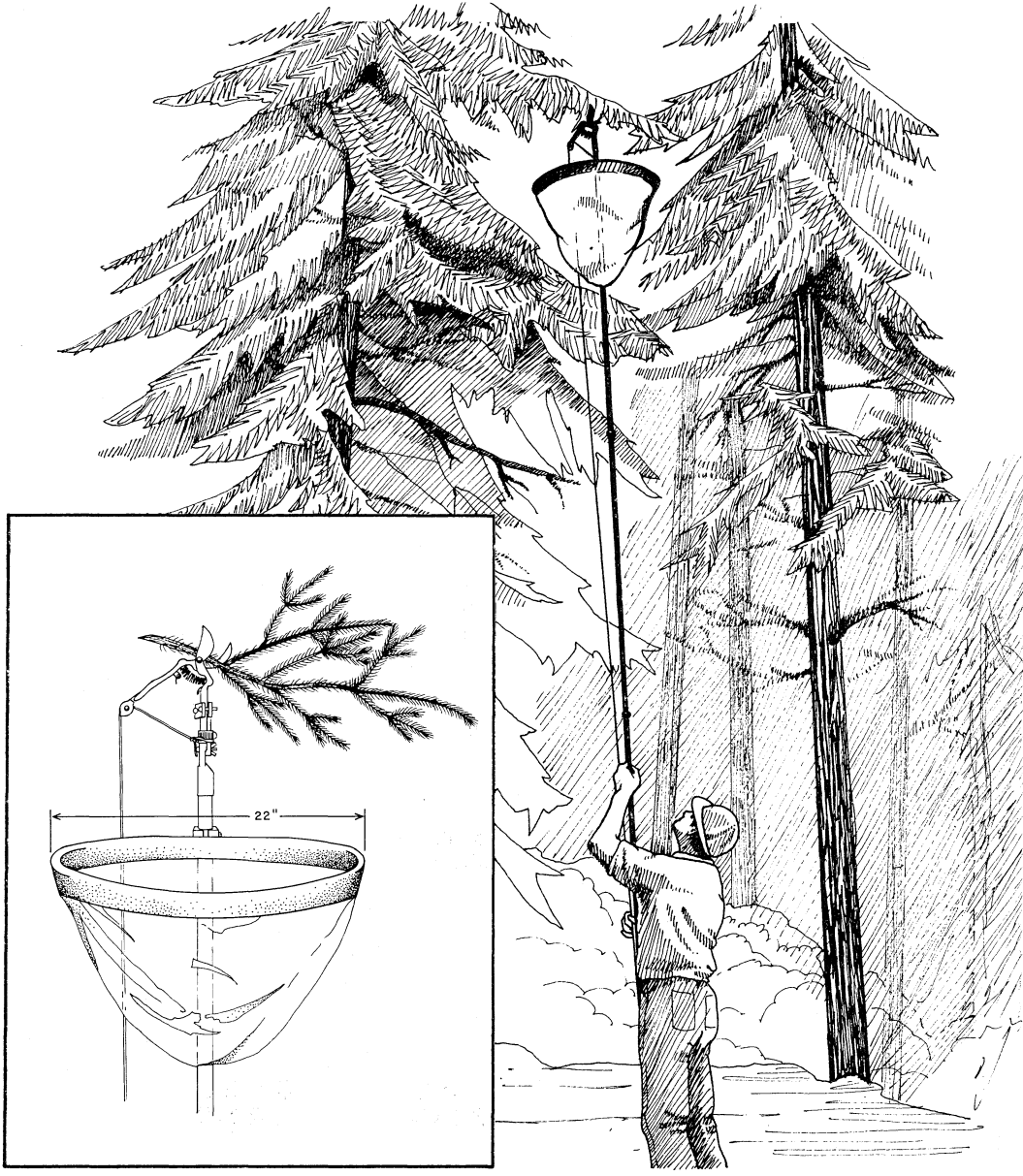
Figure 1.—The midcrown of a sample tree is that portion of the crown originating from the middle third of the trunk. For example, in a tree that is 45 feet tall, the midcrown is the area between 15 and 30 feet above the ground.

Sampling the Midcrown

The midcrown density of larvae of any instar can be estimated on a 2 ½-acre (1-hectare) plot by sampling the midcrowns of 15 trees. For a larger area, more plots with fewer trees are needed. For example, larval density is best estimated on a tract of several hundred acres or more by sampling three trees on each of 50 small randomly located plots. The mean density of larvae for the whole area is determined by averaging densities from all plots.

Procedure

1. On each plot, select host trees that can be sampled in the midcrown with a pole pruner. Such trees are usually between 20 and 50 feet tall (fig. 1).



2. Clip three branches about 18 inches long from the midcrown of each sample tree, collecting all three branches in the basket of the pruner (fig. 2). One branch should come from the outside of the crown and two branches from the inside (fig. 3).

Figure 2.—A pole pruner is a sectional pole with clippers and a basket for collecting branch samples. The pole is positioned so that when the branch is clipped it drops directly into the basket, thereby capturing all larvae on the sample. Care must be taken not to disturb the branch before clipping or larvae will drop off prematurely. The three sample branches should be collected together in the basket before lowering the pole to the ground.

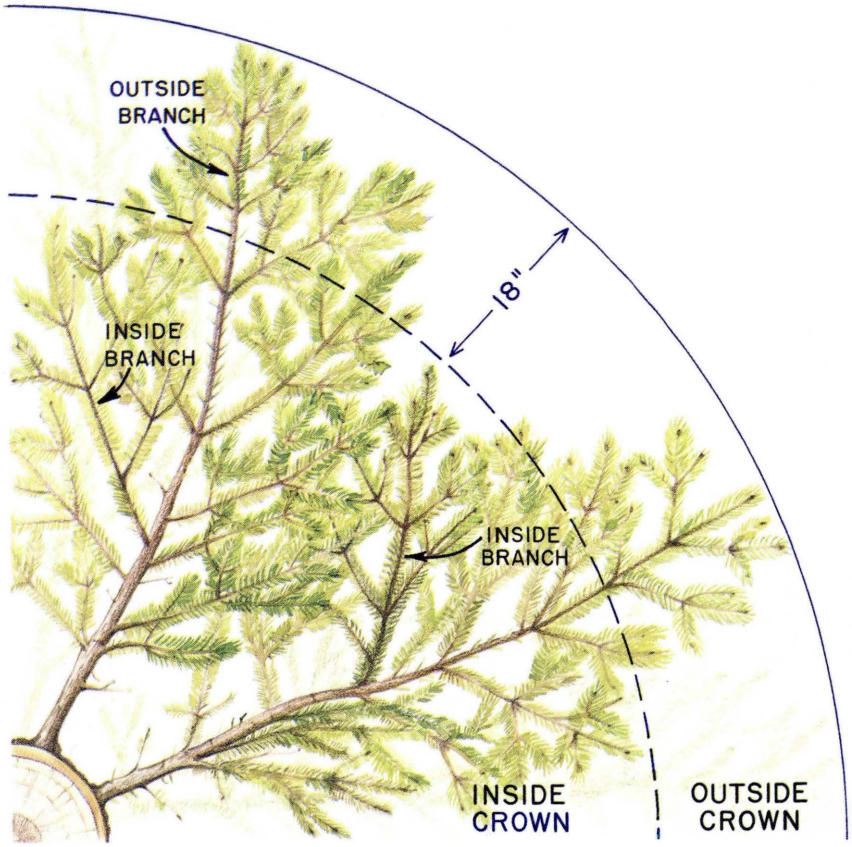


Figure 3.—The outside crown is all the foliage on the outer 18 inches of the main branches—those that grow from the tree trunk. The inside crown is the foliage on those lateral branches at least 18 inches back from the end of the main branch. The sample from a tree includes one outside branch and two inside branches.

3. Lower the basket to the ground and place the three branches on a light-colored drop cloth, making sure that any larvae in the basket are also removed. Hold each branch about 12 inches above the drop cloth and rap it several times with a short stick to dislodge the larvae (fig. 4). Record the number of larvae collected on the drop cloth.

4. Measure in inches the length and the maximum width of the foliage on each branch (fig. 5). Multiply the length by the width and divide by 2 (or use a previously prepared computation table) to determine the square-inch area of each branch. Total the areas of the three branches.

5. Divide the number of larvae on the three branches by the total branch area and multiply by 1,000. This is the number of larvae per 1,000 inch^2 in the sample.

6. Repeat steps 2–5 for each sample tree on the plot and average the results to obtain a mean density of larvae for the plot.

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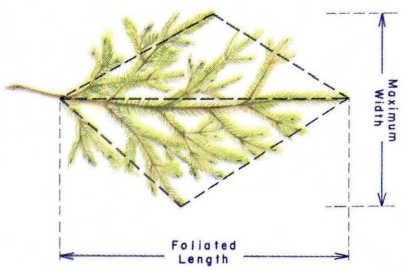

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Figure 4.—An off-white canvas about 4 × 6 feet is a satisfactory drop cloth. If the samples have a large number of larvae, grid lines can be drawn on the cloth to facilitate counting.

Figure 5.—Branch area is the area of the branch occupied by foliage. It is the area of two triangles with a common base, defined by the length and maximum width of the sample branch.

Sampling the Lower Crown

Figure 6.—A hand-held drop cloth supported in the corners by a metal frame is adequate for lower crown sampling. Larvae are observed as present or absent but are not counted.

Where larvae are scarce, that is, less than 25 percent of the branches are infested, a great deal of time is spent cutting and searching midcrown foliage without finding any larvae. In such cases more trees can be sampled much more easily by systematically examining branches in the more accessible lower crown. With certain corrections, the density of larvae in the lower crown is a satisfactory index of midcrown density. This method should be used only when sampling first and second instars because distribution changes as the larvae mature.

Low densities of larvae can be estimated quickly by simply determining the proportion of sample units that are infested. At least 100 trees should be sampled on a 5-acre (2-hectare) plot. For a larger area, a cluster of several 100-tree plots can be used or plots can be spaced throughout the area and the results averaged. Because of the ease of lower crown sampling, a large number of trees can be sampled quite rapidly. Each person can sample approximately one tree per minute if sample trees are fairly close together.

Procedure

1. On each plot, select host trees for sampling that have low foliage within reach from the ground. A tree of almost any height is acceptable so long as accessible sample branches have new growth. Avoid sampling the tops of small trees.

2. Hold a drop cloth under 18–20 inches of the branch to be sampled. Rap the branch vigorously with a short stick, being careful not to disturb other branches on the tree. Larvae will drop onto the cloth (fig. 6).

3. Examine the drop cloth for tussock moth larvae. If a larva is found, note the tree as infested and proceed to another tree. If no larva is found, continue sampling other branches on the same tree until a larva is found or until a total of three branches have been examined.

4. After approximately 100 trees have been sampled on the plot, determine the proportion infested by dividing the number of infested trees by the number of trees sampled.

5. Using table 1, convert the proportion of infested trees to estimated midcrown density.

Table 1. Table for converting the proportion of infested lower crown samples (p) to density of early larvae per 1000 square inches of midcrown branch area ($\hat{M}$)

p	$\hat{M}$	p	$\hat{M}$
0.001	0.004	0.31	1.48
0.002	0.008	0.32	1.54
0.003	0.012	0.33	1.60
0.004	0.016	0.34	1.66
0.005	0.020	0.35	1.72
0.006	0.024	0.36	1.78
0.007	0.028	0.37	1.85
0.008	0.032	0.38	1.91
0.009	0.036	0.39	1.98
0.01	0.04	0.40	2.04
0.02	0.08	0.41	2.11
0.03	0.12	0.42	2.18
0.04	0.16	0.43	2.25
0.05	0.20	0.44	2.32
0.06	0.25	0.45	2.39
0.07	0.29	0.46	2.46
0.08	0.33	0.47	2.54
0.09	0.38	0.48	2.62
0.10	0.42	0.49	2.69
0.11	0.47	0.50	2.77
0.12	0.51	0.51	2.85
0.13	0.56	0.52	2.94
0.14	0.60	0.53	3.02
0.15	0.65	0.54	3.11
0.16	0.70	0.55	3.19
0.17	0.74	0.56	3.28
0.18	0.79	0.57	3.38
0.19	0.84	0.58	3.47
0.20	0.89	0.59	3.57
0.21	0.94	0.60	3.67
0.22	0.99	0.61	3.77
0.23	1.04	0.62	3.87
0.24	1.10	0.63	3.98
0.25	1.15	0.64	4.09
0.26	1.20	0.65	4.20
0.27	1.26	0.66	4.32
0.28	1.31	0.67	4.43
0.29	1.37	0.68	4.56
0.30	1.43	0.69	4.68
		0.70	4.82

Classifying Larval Density

A forest manager does not always need to know the precise density of larvae on a plot to determine a course of action. Sometimes, only an estimate of the general level of abundance is sufficient. This can be described by a broad larval density class that is usually easier to determine than the precise estimate of density discussed earlier.

A technique called sequential sampling is used to classify larval density into general categories. It should be used in situations where more precise estimates are not necessary. For example, sequential sampling is most appropriate in determining if an insect population exceeds a certain biological or economic significance. It uses a flexible sample size rather than a fixed number of sample units on each plot.

Sequential sampling can be used to classify larval density in the midcrown by sampling either directly in the midcrown or indirectly in the lower crown. Midcrown sampling is suggested for suspected outbreaks while lower crown sampling is appropriate only for sparse populations. Sequential sampling is especially valuable in surveys for screening populations in a specific density range, but a sequential survey may need to be followed by more intensive sampling. The sequential methods are recommended only for classifying the density of first and second instars.

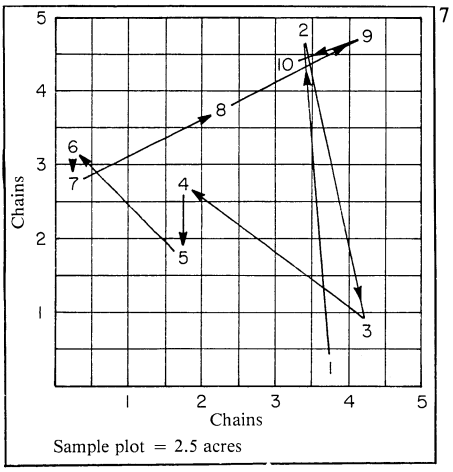

Figure 7.—Sample trees can be randomly located on a 5-chain grid using a random numbers table to locate grid coordinates. Trees must be sampled in order of their selection and not by the shortest travel route between trees.

Sample trees used in sequential sampling must be selected in a random sequence on the plot to be classified. This can be done by drawing grid lines over the plot on paper and randomly selecting the squares in which to sample a tree (fig. 7).

Sequential Sampling in the Midcrown

Sequential sampling in the midcrown is most useful at the beginning of an outbreak when small larvae are relatively common but defoliation is not yet apparent. The sequential plan separates larval density on the plot into either a light class ($\leq$10 early larvae per 1,000 inch^2) or a heavy class ($\geq$20 early larvae per 1,000 inch^2). In general, light densities of larvae will not cause noticeable loss of foliage while heavy densities, characteristic of outbreak populations, will cause conspicuous defoliation.

Procedure

1. Randomly select a host tree that can be sampled in the midcrown with a pole pruner (fig. 7). Such trees should usually be 20–50 feet tall (fig. 1).

2. Clip three branches about 18 inches long from the midcrown of each sample tree, collecting all three branches in the basket of the pruner (fig. 2). One branch should come from the outside of the crown and two branches from the inside (fig. 3).

3. Lower the basket to the ground and place the three branches on a light-colored drop cloth, making sure that any larvae in the basket are also removed. Hold each branch about 12 inches over the drop cloth and rap it several times with a short stick to dislodge the larvae (fig. 4). Record the number of larvae collected on the drop cloth.

4. Measure in inches the length and maximum width of the foliage on each branch (fig. 5). Multiply the length by the width and divide by 2 (or use a previously prepared computation table) to determine the square-inch area of each branch. Total the areas of the three branches.

5. Divide the number of larvae on the three branches by the total branch area and multiply by 1,000. This is the number of larvae per 1,000 inch^2 in the sample.

Number of trees		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	Larval density class
Sequential sampling plan		Light / Heavy		19 / 65	33 / 79	47 / 93	61 / 107	75 / 121	89 / 135	103 / 149	117 / 163	131 / 177	145 / 191	160 / 206	173 / 219	187 / 233	
Plot no.	1																
	2																
	3																
	4																
	5																
	6																
	7																
	8																

Figure 8.—Form for sequential sampling of larvae in the midcrown. The numbers in the sequential plan represent upper limits of light and lower limits of heavy larval populations.

6. Record the number of larvae per 1,000 inch^2 (larval density) found on the sample tree on the sequential form (fig. 8). After sampling a second tree, add that density number to the number found for the first tree, then record the total in the next box. Keep adding the larval density numbers from successive trees to the previous totals until a number is reached that is either lower than the upper limit for light populations or higher than the lower limits for heavy populations.

7. If the cumulative density on the first three trees sampled is equal to or less than the low value in the corner of the overhead box on the form, or equal to or more than the high value, stop sampling and classify larval density as either light or heavy, respectively. If the cumulative total falls between the specified limits in the overhead box, no classification can be made and another tree must be sampled.

8. If larval density cannot be classified after 15 trees have been sampled, stop sampling and classify the plot in the intermediate density class.

Sequential Sampling in the Lower Crown

Sequential sampling in the lower crown should be used only to evaluate sparse populations. The midcrown density of larvae on a plot is classed as either low ($\leq$one early larva per 1,000 inch^2) or suboutbreak ($\geq$three early larvae per 1,000 inch^2). At low densities, larvae are uncommon and present no risk of an outbreak for at least 2 years. At suboutbreak densities larvae have the potential to reach outbreak numbers in the next generation.

Procedure

1. Randomly select a host tree for sampling which has foliage within reach from the ground (fig. 7). A tree of any height is acceptable as long as sample branches have new growth. Avoid sampling the tops of small trees.

2. Hold a drop cloth under 18–20 inches of the branch to be sampled. Rap the branch vigorously with a short stick, being careful not to disturb other branches on the tree. Larvae will drop onto the cloth (fig. 6).

3. Examine the drop cloth for tussock moth larvae. If a larva is found, note the tree as infested and proceed to another tree. If no larva is found, continue sampling other branches on the same tree until a larva is found or until a total of three branches have been examined.

Number of trees	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	Larval density class
Sequential sampling plan	Low / Sub-outbreak			– / 4	– / 4	0 / 5	0 / 5	0 / 6	1 / 6	1 / 6	1 / 7	2 / 7	2 / 7	2 / 8	3 / 8	3 / 8	4 / 9	4 / 9	4 / 10	5 / 10	
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Figure 9.—Form for sequential sampling of larvae in the lower crown. The sequential plan is written into the squares across the top row.

4. Record the number of infested trees on the sequential form (fig. 9) by adding each one to the total number of infested trees found previously. To record a tree as uninfested, add zero to the previous number and write the figure under the appropriate number of sampled trees.

5. If the cumulative total of infested trees is equal to or less than the low value in the sequential sampling plan on the form, or equal to or more than the high value, stop sampling and classify larval density as either low or suboutbreak, respectively. If the cumulative total is between the specified limits in the overhead box, no classification can be made and another tree must be sampled.

6. If larval density is not classified after 20 trees have been sampled, stop sampling and classify the plot in the intermediate class.

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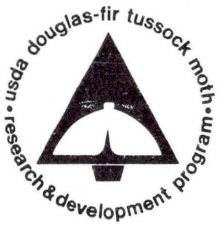

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